

SEQUENCE LISTING

<110> Maines, Mahin D.

<120> METHODS OF MODIFYING CELL STRUCTURE AND REMODELING
TISSUE

<130> 176/60981

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<150> 60/261,500

<151> 2001-01-12

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 296

<212> PRT

<213> Homo sapiens

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Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
20 25 30

Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
35 40 45

Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
50 55 60

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
65 70 75 80

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
85 90 95

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
100 105 110

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
115 120 125

Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
130 135 140

Leu Leu Lys Gly Ser Leu Leu Phe Thr Ser Asp Pro Leu Glu Glu Asp
145 150 155 160

Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
165 170 175

Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
180 185 190

Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
195 200 205

Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
210 215 220

Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
225 230 235 240

Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
245 250 255

Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
260 265 270

Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
275 280 285

Gln Lys Tyr Cys Cys Ser Arg Lys
290 295

<210> 2

<211> 1070

<212> DNA

<213> Homo sapiens

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tccgtgcgga tgagggactt gcggaatcca cacccttcct cagcgttcct gaacctgatt 180
ggcttcgtgt cgagaaggga gtcggggagc attgatggag tccagcagat ttctttggag 240
gatgctcttt ccagccaaga ggtggaggtc gcctatatct gcagtgaag ctccagccat 300
gaggactaca tcaggcagtt ccttaatgct ggcaagcacg tccttgtgga ataccccatg 360
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..... ttgcacgagg agcatgttga actcttgatg gaggaattcg ctttcctgaa aaaagaagtg 480
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..... cggtttggct tccctgcatt cagcggcatc tctcgactga cctggctggt ctcctctttt 600
..... ggggagcttt ctcttggtgc tgccactttg gaagagcgaa aggaagatca gtatatgaaa 660
..... atgacagtgt gtctggagac agagaagaaa agtccactgt catggattga agaaaaagga 720
..... cctgggtctaa aacgaaacag atatttaagc ttccatttca agtctgggtc cttggagaat 780
..... gtgccaaatg taggagtgaa taagaacata tttctgaaag atcaaaaatat atttgtccag 840
..... aaactcttgg gccagttctc tgagaaggaa ctggctgctg aaaagaaacg catcctgcac 900
..... tgccctggggc ttgcagaaga aatccagaaa tattgctgtt caaggaaagta agaggaggag 960
..... gtgatgtagc acttccaaga tggcaccagc atttggttct tctcaagagt tgaccattat 1020
..... ctctattctt aaaattaaac atgttgggga aacaaaaaaa aaaaaaaaaa 1070

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<212> PRT

<213> Homo sapiens

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..... Met Asn Thr Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
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..... Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
..... 20 25 30

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..... Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
..... 35 40 45

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..... Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
..... 50 55 60

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..... Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
..... 65 70 75 80

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..... Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
..... 85 90 95

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..... Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
..... 100 105 110

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..... Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
..... 115 120 125

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..... Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
..... 130 135 140

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..... Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu Glu
..... 145 150 155 160

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Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
 165 170 175

Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
 180 185 190

Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
 195 200 205

Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
 210 215 220

Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
 225 230 235 240

Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
 245 250 255

Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
 260 265 270

Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
 275 280 285

Gln Lys Tyr Cys Cys Ser Arg Lys
 290 295

<210> 4
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 <213> Rattus norvegicus

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Gly Arg Ala Gly Ser Val Arg Leu Arg Asp Leu Lys Asp Pro Arg Ser
 20 25 30

Ala Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu Gly
 35 40 45

Ser Leu Asp Glu Val Arg Gln Ile Ser Leu Glu Asp Ala Leu Arg Ser
 50 55 60

Gln Glu Ile Asp Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His Glu

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..... 65              70              75              80
.....
..... Asp Tyr Ile Arg Gln Phe Leu Gln Ala Gly Lys His Val Leu Val Glu
.....              85              90              95
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..... Tyr Pro Met Thr Leu Ser Phe Ala Ala Ala Gln Glu Leu Trp Glu Leu
.....              100              105              110
.....
..... Ala Ala Gln Lys Gly Arg Val Leu His Glu Glu His Val Glu Leu Leu
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..... Met Glu Glu Phe Glu Phe Leu Arg Arg Glu Val Leu Gly Lys Glu Leu
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..... Leu Lys Gly Ser Leu Arg Phe Thr Ala Ser Pro Leu Glu Glu Glu Arg
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..... Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu Val
.....              165              170              175
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..... Ser Leu Phe Gly Glu Leu Ser Leu Ile Ser Ala Thr Leu Glu Glu Arg
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..... Lys Glu Asp Gln Tyr Met Lys Met Thr Val Gln Leu Glu Thr Gln Asn
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..... Lys Gly Leu Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys Arg
.....              210              215              220
.....
..... Asn Arg Tyr Val Asn Phe Gln Phe Thr Ser Gly Ser Leu Glu Glu Val
.....              225              230              235              240
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..... Pro Ser Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asp Ile
.....              245              250              255
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..... Phe Val Gln Lys Leu Leu Asp Gln Val Ser Ala Glu Asp Leu Ala Ala
.....              260              265              270
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..... Glu Lys Lys Arg Ile Met His Cys Leu Gly Leu Ala Ser Asp Ile Gln
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..... Lys Leu Cys His Gln Lys Lys
.....              290              295
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..... <210> 5
..... <211> 1081
..... <212> DNA

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<213> Rattus norvegicus

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gaaatttgga gtggtagtgg ttggtgttgg cagagctggc tcggtgaggc tgagggactt 180
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cggcatttct cgcctgacct ggctggtctc cctcttcggg gagctttctc ttatttctgc 660
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gaacaagggc ctgctgtcat ggattgaaga gaaagggcct ggcttaaaaa gaaacagata 780
tgtaaacttc cagttcactt ctgggtccct ggaggaagtg ccaagtgtag gggtaataa 840
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<210> 6

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: hydrophobic
domain of BVR

<220>

<221> PEPTIDE

<222> (2)

<223> where X is any aa

<400> 6

Phe Xaa Val Val Val Val

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<210> 7

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: nucleotide
binding domain of BVR

<220>

<221> PEPTIDE

<222> (2)

<223> where X is any aa

<220>

<221> PEPTIDE

<222> (4)..(5)

<223> where X is any aa

<400> 7

Gly Xaa Gly Xaa Xaa Gly

1

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<210> 8

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oxidoreductase domain of BVR

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Ala Gly Leu His Val Leu Val Glu

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<210> 9

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: leucine
zipper of BVR

<220>

<221> PEPTIDE

<222> (2)..(7)

<223> where X is any aa

<220>

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..... <222> (9)..(14)
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..... <220>
..... <221> PEPTIDE
..... <222> (16)..(21)
..... <223> where X is any aa
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..... <220>
..... <221> PEPTIDE
..... <222> (23)..(28)
..... <223> where X is any aa
.....
..... <400> 9
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.....      1              5              10              15
.....
..... Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu
.....      20              25
.....
..... <210> 10
..... <211> 3
..... <212> PRT
..... <213> Artificial Sequence
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..... <220>
..... <223> Description of Artificial Sequence:  kinase motif
.....          of BVR
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..... <400> 10
..... Ser Arg Arg
.....      1
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..... <210> 11
..... <211> 3
..... <212> PRT
..... <213> Artificial Sequence
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..... <220>
..... <223> Description of Artificial Sequence:  kinase motif
.....          of BVR
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..... <400> 11
..... Lys Gly Ser
.....      1

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<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: kinase motif
of BVR

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<221> PEPTIDE
<222> (3)
<223> where X is any aa

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Phe Thr Xaa
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<210> 13
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nuclear
localization signal of BVR

<400> 13
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1 5

<210> 14
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: methylation
site of BVR

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Pro Gly Leu Lys Arg
1 5

<210> 15

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: zinc finger
domain of BVR

<220>

<221> PEPTIDE

<222> (3)..(12)

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<210> 16

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<212> PRT

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<223> Description of Artificial Sequence: protein
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<221> PEPTIDE

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<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: protein
kinase C inhibiting domain

<223> where X is any aa

<223> where X is any aa

Gln Lys Xaa Cys Xaa Xaa Xaa Lys

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